

#3

<110> Shimkets, Richard Fernandes, Elma Vernet, Corine Yang, Meijia Boldog, Ferenc Herrmann, John

<120> Novel Nucleic Acid Sequences Encoding Human Semaphorin-Like Polypeptides

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<150> 09/604,286

<151> 2000-06-22

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<170> PatentIn Ver. 2.0

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ctc ttg gac gag gac acc ctc ttt tgc cag ggc ctt gaa gtt ttc tac 262 Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val Phe Tyr 35 40 45 50

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gcc act Ala Thr													254
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gat cag Asp Glr	_				_	_							446
gtg ctt Val Leu					-		 _		_	_		_	494
aac gcc Asn Ala 145	Pro			_	_			_		_		-	542
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Ser Thr Lys Asp Thr Ile Trp Leu Val Val Ala Phe Ser Asn Ala Ser 65 70 75 80

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Gln Leu Leu Thr Asp Gly His Tyr Met Thr Leu Pro Leu Ser Leu Asp 100 105 110

Gln Leu Pro Cys Glu Asp Leu Thr Gly Gly Ser Gly Gly Val Pro Val 115 120 125

Leu Arg Val Gly Asn Asp Phe Gly Cys Tyr Gln Arg Pro Tyr Cys Asn 130 135 140

Ala Pro Leu Pro Ser Gln Gly Pro Tyr Ser Val Lys Phe Leu Val Met 145 150 155 160

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Tyr Leu His Gln Gly Lys Asn Pro Asn Ser Ile Asp Thr Trp Pro Gly
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	atc Ile															581
	aca Thr					_										629
	ttt Phe															677
	gta Val 140															725
	aat Asn															773
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Asp Gln Asp Lys Gly Asp Gly Ser Leu Lys Tyr Ile Leu Ser Gly Asp 85 90 95

Gly Ala Gly Thr Leu Phe Ile Ile Asp Glu Lys Thr Gly Asp Ile His
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Ala Thr Arg Arg Ile Asp Arg Glu Glu Lys Ala Phe Tyr Thr Leu Arg 115 120 125

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Glu Phe Val Ile Lys Ile His Asp Ile Asn Asp Asn Glu Pro Thr Phe 145 150 155 160

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Thr Ser Val Val Gln Val Thr Ala Thr Asp Ala Asp Asp Pro Ser Tyr 180 185 190

Gly Asn Ser Ala Arg Val Ile Tyr Ser Ile Leu Gln Gly Gln Pro Tyr 195 200 205

Phe Ser Val Glu Pro Glu Thr Gly Ile Ile Arg Thr Ala Leu Pro Asn 210 215 220

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Ile Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Pro Gln Asn 260 265 270

Thr Ile His Leu Arg Val Leu Glu Ser Ser Pro Val Gly Thr Ala Ile 275 280 285

Gly Ser Val Lys Ala Thr Asp Ala Asp Thr Gly Lys Asn Ala Glu Val 290 295 300

Glu Tyr Arg Ile Ile Asp Gly Asp Gly Thr Asp Met Phe Asp Ile Val 305 310 315 320

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650

645

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						aag Lys		_	_	_					-	1688
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Glu Pro Pro Val Phe Ser Arg Ser Ser Tyr Leu Phe Glu Val His Glu
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Asp Ile Glu Val Gly Thr Ile Ile Gly Thr Val Met Ala Arg Asp Pro
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Asp Ser Ile Ser Ser Pro Ile Arg Phe Ser Leu Asp Arg His Thr Asp 100 105 110

Leu Asp Arg Ile Phe Asn Ile His Ser Gly Asn Gly Ser Leu Tyr Thr
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Ser Lys Pro Leu Asp Arg Glu Leu Ser Gln Trp His Asn Ser Leu Val 130 135 140

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Phe Val Arg Ile Leu Asp Val Asn Asp Asn Ala Pro Gln Phe Ala Val 165 170 175

Phe Tyr Asp Thr Phe Val Cys Glu Asn Ala Arg Pro Gly Gln Leu Ile 180 185 190

Gln Thr Ile Ser Ala Val Asp Lys Asp Pro Leu Gly Gln Lys 195 200 205

Phe Phe Phe Ser Leu Ala Ala Val Asn Pro Asn Phe Thr Val Gln Asp 210 215 220

Asn Glu Asp Asn Thr Ala Arg Ile Leu Thr Arg Lys Asn Gly Phe Asn 225 230 235 240

Arg His Glu Ile Ser Thr Tyr Leu Leu Pro Val Val Ile Ser Asp Asn 245 250 255



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Ala Cys Asp 275

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Cys Ile Ile Ile Leu Leu Val Ile Val Val Leu Phe Ala Ala Leu Lys 305 310 315 320

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Gln Ala Phe Asp Ile Gly Thr Leu Arg Asn Pro Ala Ala Ile Glu Glu 355 360 365

Lys Lys Leu Arg Arg Asp Ile Ile Pro Glu Thr Leu Phe Ile Pro Arg 370 375 380

Arg Thr Pro Thr Ala Pro Asp Asn Thr Asp Val Arg Asp Phe Ile Asn 385 390 395 400

Glu Arg Leu Lys Glu His Asp Leu Asp Pro Thr Ala Pro Pro Tyr Asp 405 410 415

Ser Leu Ala Thr Tyr Ala Tyr Glu Gly Asn Asp Ser Ile Ala Glu Ser 420 425 430

Leu Ser Ser Leu Glu Ser Gly Thr Thr Glu Gly Asp Gln Asn Tyr Asp
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					gtc Val											381
					cag Gln											429
					gga Gly											477
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	gta Val															1389
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1508

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Glu Phe Phe Ile Gln Asn Asp Gln Cys Gln Glu Met Asp Thr Thr Thr 50 55 60

Asp Lys Trp Val Lys Leu Thr Asp Asn Gly Glu Trp Gly Ser His Ser 65 70 75 80

Val Met Leu Lys Ser Gly Thr Asn Ile Leu Tyr Trp Arg Thr Thr Gly
85 90 95

Ile Leu Met Gly Ser Lys Ala Val Lys Pro Val Leu Val Lys Asn Ile
100 105 110

Thr Ile Glu Gly Val Ala Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro 115 120 125

Gly Thr Phe Ser Asn Lys Pro Gly Ser Phe Asn Cys Gln Val Cys Pro 130 135 140

Arg Asn Thr Tyr Ser Glu Lys Gly Ala Lys Glu Cys Ile Arg Cys Lys 145 150 155 160

Asp Asp Ser Gln Phe Ser Glu Glu Gly Ser Ser Glu Cys Thr Glu Arg 165 170 175

Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile His Thr Pro Cys Asp 180 185 190

Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp Ile Glu Pro Lys Ile 195 200 205

Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu Pro Pro Ser Gly Glu 210 215 220

Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe Tyr Asn Asn Gly Ser 225 230 235 240

Ser Ser Cys His Pro Cys Pro Pro Gly Thr Phe Ser Asp Gly Thr Lys



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Gly Ala Thr Gly Ser Glu Leu Gly Arg Ile Thr Phe Val Phe Glu Thr 340 345 350

Leu Cys Ser Ala Asp Cys Val Leu Tyr Phe Met Val Asp Ile Asn Arg 355 360 365

Lys Ser Thr Asn Val Val Glu Ser Trp Gly Gly Thr Lys Glu Lys Gln 370 380

Ala Tyr Thr His Ile Ile Phe Lys Asn Ala Thr Phe Thr Phe Thr Trp 385 390 395 400

Gly Ile Pro Arg Glu Leu Ile Gln Gly Pro Arg
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5 10 15 20

gct gag gtg tgg tgg aac ctt gtg ccg cgt aag aca gtg tct tct ggg 273 Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr Val Ser Ser Gly

1

25 30 35

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			acg Thr					369
			gcc Ala 75					417
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			cag Gln					513
			tcc Ser					561
			tac Tyr					609
			999 Gly 155					657
			ctt Leu					705
			acg Thr					753
			aca Thr					801
			gcc Ala					849
			gtc Val 235					897
			gag Glu					945



												tgg Trp 275	993
												cag Gln	1041
												tcc Ser	1089
												gac Asp	1137
												cgg Arg	1185
												tgg Trp 355	1233
_		_		_		_				_	_	att Ile	1281
												ccc Pro	1329
												cag Gln	1377
												aac Asn	1425
												acc Thr 435	1473
												gct Ala	1521
_	-			_		_	_					ttt Phe	1569
_		_	_	_	_			_	_			ctg Leu	1617



ttt gcc ggc tcc cgc tct cag ctg gtg cag ctg ccc gtg gcc gac tgc 1665 Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro Val Ala Asp Cys 485 490 495 500
ata aag tat cgc tcc tgt gca gac tgt gtc ctc gcc cgg gac ccc tat 1713 Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala Arg Asp Pro Tyr 505 510 515
tgc gcc tgg agc gtc aac acc agc cgc tgt gtg gcc gtg ggt ggc cac 1761 Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala Val Gly Gly His 520 525 530
ttt gga tct tta ctg atc cag cat gtg atg acc tcg gac act tca ggc 1809 Phe Gly Ser Leu Leu Ile Gln His Val Met Thr Ser Asp Thr Ser Gly 535 540 545
att tgc aac ctc cgt ggc agt aag aaa gtc agg ccc act ccc aaa aac 1857 Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro Thr Pro Lys Asn 550 555 560
atc acg gtg gtg gcg ggc aca gac ctg gtg ctg ccc tgc cac ctc tcc 1905 Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu Pro Cys His Leu Ser 565 570 575 580
tcc act tgg ccc cgg ggt tca gtg gta ttt taaacttgcc ttcttcctgt 1955 Ser Thr Trp Pro Arg Gly Ser Val Val Phe 585 590
acagggctgg gaaaggctgt gttaggggaa aaaaaggaaa gggtgggcct gctgtggaca 2015
atggcatact ctcttccagc cctaggagga gggctcctaa cagtgtaact tattgtgtcc 2075
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Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu 50 55 60
Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala 65 70 75 80

Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro 155 150 Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu 170 165 Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu 185 Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe 195 Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser Val Gly Ser Phe Thr Gly Asp Asp Lys Val Tyr Phe Phe Phe Arg 230 Glu Arg Ala Val Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg 245 250 Val Ala Arg Val Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln 265 Arg Lys Trp Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro 280 275 Asn Trp Gln Leu Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln Asp Thr Ser Trp His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln Trp Gly Asp Met Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu 325 Ile Gln Arg Val Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala Gln Lys Trp Asp Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly 360

370

380

Ser Cys Ile Asn Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu

375

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390
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Gly Thr Asn Phe Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp
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Gly Ala Thr Tyr Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu
                             440
Leu Lys Ala Val Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu
                        455
Gln Leu Phe Asp Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser
465
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                                         475
Lys Lys Leu Leu Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro
                485
                                    490
Val Ala Asp Cys Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala
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Arg Asp Pro Tyr Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala
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Val Gly Gly His Phe Gly Ser Leu Leu Ile Gln His Val Met Thr Ser
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Asp Thr Ser Gly Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro
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                                         555
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attqtctqcq ctqqqqaaqq qqacaqqccq qqaccqqgac ctccqctcgc agccggccgc 120 accagcagga cagctggcct gaagctcaga gccggggcgt gcgcc atg gcc cca cac 177 Met Ala Pro His tgg gct gtc tgg ctg ctg gca gca agg ctg tgg ggc ctg ggc att ggg Trp Ala Val Trp Leu Leu Ala Ala Arg Leu Trp Gly Leu Gly Ile Gly get gag gtg tgg tgg aac ett gtg eeg egt aag aca gtg tet tet ggg Ala Glu Val Trp Trp Asn Leu Val Pro Arg Lys Thr Val Ser Ser Gly 25 gag etg ged acg gta gta egg egg tte tee eag ace gge ate eag gae Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr Gly Ile Gln Asp 40 45 ttc ctg aca ctg acg ctg acg gag ccc act ggg ctt ctg tac gtg ggc Phe Leu Thr Leu Thr Glu Pro Thr Gly Leu Leu Tyr Val Gly 55 60 gcc cga gag gcc ctg ttt gcc ttc agc atg gag gcc ctg gag ctg caa Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala Leu Glu Leu Gln 70 75 gga gcg atc tcc tgg gag gcc ccc gtg gag aag aag act gag tgt atc 465 Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys Thr Glu Cys Ile cag aaa ggg aag aac aac cag acc gag tgc ttc aac ttc atc cgc ttc Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn Phe Ile Arg Phe ctg cag ccc tac aat gcc tcc cac ctg tac gtc tgt ggc acc tac gcc 561 Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys Gly Thr Tyr Ala 120 ttc cag ccc aag tgc acc tac gtc aac atg ctc acc ttc act ttg gag 609 Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr Phe Thr Leu Glu 135 140 657 cat gga gag ttt gaa gat ggg aag ggc aag tgt ccc tat gac cca gct His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro Tyr Asp Pro Ala 150 155 aag ggc cat gct ggc ctt ctt gtg gat ggt gag ctg tac tcg gcc aca 705 Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu Tyr Ser Ala Thr 180 165 170 ctc aac aac ttc ctg ggc acg gaa ccc att atc ctg cgt aac atg ggg Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu Arg Asn Met Gly 185 190 ccc cac cac tcc atg aag aca gag tac ctg gcc ttt tgg ctc aac gaa 801 Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe Trp Leu Asn Glu

200 205 210

										agt Ser					849
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_	_	_	_		_	_	_			ccg Pro					1041
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						_				cag Gln 320					1137
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			-					_		ctg Leu					1329
										atg Met 400					1377
			_	_		_			_	aag Lys					1425
		~-~				~++	202	gga	att	ast.	~~~	acc	200	+ - +	1473



·	
aca gtg ctg ttc att ggc aca gga gac ggc tgg ctg ctc aag gct gtg Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu Leu Lys Ala Val 440 445 450	1521
agc ctg ggg ccc tgg gtt cac ctg att gag gag ctg cag ctg ttt gac Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu Gln Leu Phe Asp 455 460 465	1569
cag gag ccc atg aga agc ctg gtg cta tct cag agc aag aag ctg ctc Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser Lys Lys Leu Leu 470 475 480	1617
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Val Ser Ser Gly Glu Leu Ala Thr Val Val Arg Arg Phe Ser Gln Thr 35 40 45

Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu
50 55 60

Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala 65 70 75 80

Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys
85 90 95

Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn
100 105 110

Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys 115 120 125

Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr 130 135 140

Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro 145 150 155 160

Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu 165 170 175

Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu 180 185 190

Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe 195 200 205

Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser 210 215 220

Val Gly Ser Phe Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Arg 225 230 235 240

Glu Arg Ala Val Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg 245 250 255

Val Ala Arg Val Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln



260 265. 270

Arg Lys Trp Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro 280 275 Asn Trp Gln Leu Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln 295 Asp Thr Ser Trp His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln 310 315 Trp Gly Asp Met Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu Ile Gln Arg Val Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala Gln Lys Trp Asp Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly Ser Cys Ile Asn Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu 370 Glu Leu Pro Asp Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met 390 395 Glu Glu Gln Val Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys 410 Gly Thr Asn Phe Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp 420 425 Gly Ala Thr Tyr Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu Leu Lys Ala Val Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu 450 455 Gln Leu Phe Asp Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser Lys Lys Leu Leu Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro 490 Val Ala Asp Cys Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala 500 Arg Asp Pro Tyr Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala 520 Val Gly Gly His Phe Gly Ser Leu Leu Ile Gln His Val Met Thr Ser 530 Asp Thr Ser Gly Ile Cys Asn Leu Arg Gly Ser Lys Ile Gln Ser Gly



545

Pro Xaa Pro Lys Asn Ile Thr Val Val Ala Gly Thr Asp Leu Val Leu

560

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570

575

565

510

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Ser	Leu	Gly	Asp	Met 110	Thr	Lys	Glu	Glu	Ala 115	Met	Ile	Ala	Tyr	Val 120	Glu	
											act Thr					558
_	_	-	_	_						_	att Ile					606
											cga Arg 165					654
											act Thr					702
											gac Asp					750
											gga Gly					798
		_	_		_	_	_	_			gac Asp					846
											ggc Gly 245					894
											aat Asn					942
											caa Gln					990
											cat His					1038
			_		_		_	_			agt Ser					1086
											tta Leu 325					1134
						_					ggt Gly					1182



330	335		340	345
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Asn Gly Asn I			gca gtt gaa gga Ala Val Glu Gly 375	Lys Gly
			aat aac agc gga Asn Asn Ser Gly 390	
			gaa ttc tct aat Glu Phe Ser Asn 405	
			agc gaa gga acc Ser Glu Gly Thr 420	
			cgc tgg ggc tcc Arg Trp Gly Ser	
Gly Ser Arg G			gcc ctc gtg ctg Ala Leu Val Leu 455	Met Arg
		_	aga ctg cag aaa Arg Leu Gln Lys 470	
			aca tca aca ttg Thr Ser Thr Leu 485	
		Arg Pro Ser	tgg tgg ccc ttc Trp Trp Pro Phe 500	
			tgg cct ttt att Trp Pro Phe Ile	
Trp Leu Val Ty			aga aga aaa ctg Arg Arg Lys Leu 535	Asn
tgagggaaaa tg	gtgttttc ctcaa	gaaga ctactgg	aac tggatgacct	cagaatgaac 1815
tggattgtgg tg	ttcacaag aaaat	cttag tttgtga	tga ttacattgct	ttttgttgtc 1875
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Cys Cys Leu Ile Pro Ala Asp Arg Pro Trp Asp Arg Gly Gln His Trp
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Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu
Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Gly Ser Phe Gln
                         55
Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala
Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile
Gly Arg Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys
                                105
                                                     110
            100
Glu Glu Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu
                            120
        115
Thr Met Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly
                        135
Pro Phe Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp
145
                    150
Ile Thr Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu
Gly Asn Val Leu Thr Ser Thr Pro Asn Ala Lys Thr Val Asn Gly Lys
                                                     190
            180
                                185
Ala Glu Ser Ser Asp Ser Gly Ala Glu Ser Glu Glu Glu Ala Gln
Glu Glu Val Lys Gly Ala Glu Gln Ser Asp Asn Asp Lys Lys Met Met
                        215
Lys Lys Ser Ala Asp His Lys Asn Leu Glu Val Ile Val Thr Asn Gly
                                                             240
225
                                        235
Tyr Asp Lys Asp Gly Phe Val Gln Asp Ile Gln Asn Asp Ile His Ala
                245
                                    250
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Ser Ser Ser Leu Asn Gly Arg Ser Thr Glu Glu Val Lys Pro Ile Asp 260 265 270 Glu Asn Leu Gly Gln Thr Gly Lys Ser Ala Val Cys Ile His Gln Asp 275 280 Ile Asn Asp Asp His Val Glu Asp Val Thr Gly Ile Gln His Leu Thr 295 300 Ser Asp Ser Asp Ser Glu Val Tyr Cys Asp Ser Met Glu Gln Phe Gly 310 315 Gln Glu Glu Ser Leu Asp Ser Phe Thr Ser Asn Asn Gly Pro Phe Gln 325 330 335 Tyr Tyr Leu Gly Gly His Ser Ser Gln Pro Met Glu Asn Ser Gly Phe 345 Arg Glu Asp Ile Gln Val Pro Pro Gly Asn Gly Asn Ile Gly Asn Met 360 Gln Val Val Ala Val Glu Gly Lys Gly Glu Val Lys His Gly Gly Glu 370 375 Asp Gly Arg Asn Asn Ser Gly Ala Pro His Arg Glu Lys Arg Gly Gly Glu Thr Asp Glu Phe Ser Asn Val Arg Arg Gly Arg Gly His Arg Met 410 Gln His Leu Ser Glu Gly Thr Lys Gly Arg Gln Val Gly Ser Gly Gly 420 Asp Gly Glu Arg Trp Gly Ser Asp Arg Gly Ser Arg Gly Ser Leu Asn 440 Glu Gln Ile Ala Leu Val Leu Mét Arg Leu Gln Glu Asp Met Gln Asn 450 455 Val Leu Gln Arg Leu Gln Lys Leu Glu Met Leu Thr Ala Leu Gln Ala Lys Ser Ser Thr Ser Thr Leu Gln Thr Ala Pro Gln Pro Thr Ser Gln 495 485 490 Arg Pro Ser Trp Trp Pro Phe Glu Met Ser Pro Gly Val Leu Thr Phe 500 505 Ala Ile Ile Trp Pro Phe Ile Ala Gln Trp Leu Val Tyr Leu Tyr Tyr

520

535



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cc atg gca tcc ccc aga acc gta act att gtg gcc ctc tca gtg gcc Met Ala Ser Pro Arg Thr Val Thr Ile Val Ala Leu Ser Val Ala 1 5 10 15															167	
_					_		_			atc Ile		_				215
										cgt Arg						263
_	_	_			_	_	_		_	Gly ggg						311
										gcc Ala						359
										gcc Ala 90						407
										cag Gln						455
		_		_		_	_			gga Gly		_			_	503
										cgg Arg						551
										tcc Ser						599
	_				aag Lys 165		tca Ser	taga	aaaa							630



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<213> Homo sapiens

<400> 18

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Gly Leu Phe Phe Val Phe Met Gly Thr Ile Lys Leu Thr Pro Arg Leu 20 25 30

Ser Lys Asp Ala Tyr Ser Glu Met Lys Arg Ala Tyr Lys Ser Tyr Val 35 40 45

Arg Ala Leu Pro Leu Leu Lys Lys Met Gly Ile Asn Ser Ile Leu Leu 50 55 60

Arg Lys Ser Ile Gly Ala Leu Glu Val Ala Cys Gly Ile Val Met Thr
65 70 75 80

Leu Val Pro Gly Arg Pro Lys Asp Val Ala Asn Phe Phe Leu Leu Leu 85 90 95

Leu Val Leu Ala Val Leu Phe Phe His Gln Leu Val Gly Asp Pro Leu 100 105 110

Lys Arg Tyr Ala His Ala Leu Val Phe Gly Ile Leu Leu Thr Cys Arg 115 120 125

Leu Leu Ile Ala Arg Lys Pro Glu Asp Arg Ser Ser Glu Lys Lys Pro 130 135 140

Leu Pro Gly Asn Ala Glu Glu Gln Pro Ser Leu Tyr Glu Lys Ala Pro 145 150 155 160

Gln Gly Lys Val Lys Val Ser 165

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<211> 1737

<212> DNA

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<220>

<221> CDS

<222> (296)..(1687)

<220>

<221> variation

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<223> N may be any nucleotide

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tggctccagg tggagagttg ccattccaaa ttctgcagtg gactgctctg gcctgcctga 240 cccaqtgaga ggcaaagaat gcactttctc ctgtgcttct ggagagtatc tagaa atg Met 1 aag aac cag gta tgc agt aag tgt ggt gaa ggc acc tat tcc ttg ggc 346 Lys Asn Gln Val Cys Ser Lys Cys Gly Glu Gly Thr Tyr Ser Leu Gly agt ggc atc aaa ttt gat gaa tgg gat gaa ttg ccg gca gga ttt tct 394 Ser Gly Ile Lys Phe Asp Glu Trp Asp Glu Leu Pro Ala Gly Phe Ser 25 aac atc gca aca ttc atg gac act gtg gtg ggc cct tct gac agc agg Asn Ile Ala Thr Phe Met Asp Thr Val Val Gly Pro Ser Asp Ser Arg 35 40 490 cca gac ggc tgt aac aac tct tct tgg atc cct cgt gga aac tac ata Pro Asp Gly Cys Asn Asn Ser Ser Trp Ile Pro Arg Gly Asn Tyr Ile 50 55 gaa tot aat ogt gat gac tgc acg gtg tot ttg atc tat got gtg cac 538 Glu Ser Asn Arq Asp Asp Cys Thr Val Ser Leu Ile Tyr Ala Val His 70 586 ctt aag aag tca ggc tat gtc ttc ttt gag tac cag tat gtc gac aac Leu Lys Lys Ser Gly Tyr Val Phe Phe Glu Tyr Gln Tyr Val Asp Asn aac atc ttc ttt gag ttc ttt att caa aat gat cag tgc cag gag atg 634 Asn Ile Phe Phe Glu Phe Phe Ile Gln Asn Asp Gln Cys Gln Glu Met 682 gac acc act gac aag tgg gta aaa ctt aca gac aat gga gaa tgg Asp Thr Thr Asp Lys Trp Val Lys Leu Thr Asp Asn Gly Glu Trp 120 ggc tct cat tct gta atg ctg aaa tca ggc aca aac ata ctc tac tgg 730 Gly Ser His Ser Val Met Leu Lys Ser Gly Thr Asn Ile Leu Tyr Trp 130 135 aga act aca ggc atc ctt atg ggt tct aag gcg gtc aag cct gtg ctg 778 Arg Thr Thr Gly Ile Leu Met Gly Ser Lys Ala Val Lys Pro Val Leu 160 150 gta aaa aat atc aca att gaa ggg gtg gcg tac aca tca gaa tgt ttt Val Lys Asn Ile Thr Ile Glu Gly Val Ala Tyr Thr Ser Glu Cys Phe 165 175 cct tgc aag cca ggc aca ttc agc aac aaa cca ggt tca ttc aac tgc Pro Cys Lys Pro Gly Thr Phe Ser Asn Lys Pro Gly Ser Phe Asn Cys 180 190 cag gtg tgt ccc aga aac acc tat tct gag aaa gga gcc aaa gaa tgt



Gln Val Cys Pro Arg Asn Thr Tyr Ser Glu Lys Gly Ala Lys Glu Cys

	195					200					205					
		_		_	-		caa Gln				_			_		970
_			_			-	acc Thr									1018
							aag Lys									1066
				_			gat Asp 265			_	_		_	_		1114
							tgt Cys									1162
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							aat Asn 345									1354
							atc Ile									1402
	_		_				ttg Leu									1450
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							aat Asn 425									1594

aaa qaa aaa caa gct tac acc cat atc atc ttc aag aat gca act ttt 1642 Lys Glu Lys Gln Ala Tyr Thr His Ile Ile Phe Lys Asn Ala Thr Phe 440 435 aca ttt aca tgg ggc att ccc aga gaa cta att cag ggt cca aga 1687 Thr Phe Thr Trp Gly Ile Pro Arg Glu Leu Ile Gln Gly Pro Arg taataqacqq ttccnccatt gacatgtttg aaggatttat tcctattcac 1737 <210> 20 <211> 464 <212> PRT <213> Homo sapiens <400> 20 Met Lys Asn Gln Val Cys Ser Lys Cys Gly Glu Gly Thr Tyr Ser Leu Gly Ser Gly Ile Lys Phe Asp Glu Trp Asp Glu Leu Pro Ala Gly Phe 25 Ser Asn Ile Ala Thr Phe Met Asp Thr Val Val Gly Pro Ser Asp Ser 40 Arg Pro Asp Gly Cys Asn Asn Ser Ser Trp Ile Pro Arg Gly Asn Tyr Ile Glu Ser Asn Arg Asp Asp Cys Thr Val Ser Leu Ile Tyr Ala Val 70 75 His Leu Lys Lys Ser Gly Tyr Val Phe Phe Glu Tyr Gln Tyr Val Asp Asn Asn Ile Phe Phe Glu Phe Phe Ile Gln Asn Asp Gln Cys Gln Glu 105 Met Asp Thr Thr Asp Lys Trp Val Lys Leu Thr Asp Asn Gly Glu 125 115 120 Trp Gly Ser His Ser Val Met Leu Lys Ser Gly Thr Asn Ile Leu Tyr 135 130 Trp Arg Thr Thr Gly Ile Leu Met Gly Ser Lys Ala Val Lys Pro Val 150 155 Leu Val Lys Asn Ile Thr Ile Glu Gly Val Ala Tyr Thr Ser Glu Cys Phe Pro Cys Lys Pro Gly Thr Phe Ser Asn Lys Pro Gly Ser Phe Asn Cys Gln Val Cys Pro Arg Asn Thr Tyr Ser Glu Lys Gly Ala Lys Glu



200

Cys Ile Arg Cys Lys Asp Asp Ser Gln Phe Ser Glu Glu Gly Ser Ser Glu Cys Thr Glu Arg Pro Pro Cys Thr Thr Lys Asp Tyr Phe Gln Ile 230 235 His Thr Pro Cys Asp Glu Glu Gly Lys Thr Gln Ile Met Tyr Lys Trp 250 Ile Glu Pro Lys Ile Cys Arg Glu Asp Leu Thr Asp Ala Ile Arg Leu 260 Pro Pro Ser Gly Glu Lys Lys Asp Cys Pro Pro Cys Asn Pro Gly Phe 280 Tyr Asn Asn Gly Ser Ser Ser Cys His Pro Cys Pro Pro Gly Thr Phe 295 Ser Asp Gly Thr Lys Glu Cys Arg Pro Cys Pro Ala Gly Thr Glu Pro Ala Leu Gly Phe Glu Tyr Lys Trp Trp Asn Val Leu Pro Gly Asn Met 330 Lys Thr Ser Cys Phe Asn Val Gly Asn Ser Lys Cys Asp Gly Met Asn 340 350 Gly Trp Glu Val Ala Gly Asp His Ile Gln Ser Gly Ala Gly Gly Ser 360 Asp Asn Asp Tyr Leu Ile Leu Asn Leu His Ile Pro Gly Phe Lys Pro 375 Pro Thr Ser Met Thr Gly Ala Thr Gly Ser Glu Leu Gly Arg Ile Thr 385 390 400 Phe Val Phe Glu Thr Leu Cys Ser Ala Asp Cys Val Leu Tyr Phe Met 410 Val Asp Ile Asn Arg Lys Ser Thr Asn Val Val Glu Ser Trp Gly Gly

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Phe Thr Phe Thr Trp Gly Ile Pro Arg Glu Leu Ile Gln Gly Pro Arg

455



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460

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165	170	175	180
ctc aac aac ttc ctg Leu Asn Asn Phe Leu 185	Gly Thr Glu Pro		
ccc cac cac tcc atg Pro His His Ser Met 200		Leu Ala Phe Trp I	
cct cac ttt gta ggc Pro His Phe Val Gly 215			
acg ggg gac gac gac Thr Gly Asp Asp Asp 230			
gag tcc gac tgc tat Glu Ser Asp Cys Tyr 245			
tgc aag ggc gat atg Cys Lys Gly Asp Met 265			
acg ttc ctg aag gcg Thr Phe Leu Lys Ala 280		s Ser Ala Pro Asn T	
tac ttc aac cag ctg Tyr Phe Asn Gln Leu 295			
cac aac acc acc ttc His Asn Thr Thr Phe 310			
tac ctg tcg gcc atc Tyr Leu Ser Ala Ile 325			
ttt gag ggc ccc tat Phe Glu Gly Pro Tyr 345			
cgc tac act gac cct Arg Tyr Thr Asp Pro 360	_	Arg Pro Gly Ser C	· - ·
aac tgg cat cgg cgc Asn Trp His Arg Arg 375			
aac atc ctc aac ttc Asn Ile Leu Asn Phe 390			

Pr

						ccc Pro									1425
						cgg Arg									1473
						aca Thr									1521
_	_				-	cac His									1569
						ctg Leu 475									1617
						cag Gln									1665
	-		_		_	gca Ala	_	-	-		_		_		1713
						acc Thr									1761
				_		cag Gln			_		_	_			 1809
						agt Ser 555									1857
						aca Thr									1905
						tca Ser		_				_			1953
_	_					ctg Leu									2001
_	_	_				cat His				_		tagg	gagga	igg	2047

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tttttatatt gacaaataaa atggagaaaa tgaaaaaaaa aaaaaaaaa 2156

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<213> Homo sapiens

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Gly Ile Gln Asp Phe Leu Thr Leu Thr Leu Thr Glu Pro Thr Gly Leu
50 55 60

Leu Tyr Val Gly Ala Arg Glu Ala Leu Phe Ala Phe Ser Met Glu Ala 65 70 75 80

Leu Glu Leu Gln Gly Ala Ile Ser Trp Glu Ala Pro Val Glu Lys Lys 85 90 95

Thr Glu Cys Ile Gln Lys Gly Lys Asn Asn Gln Thr Glu Cys Phe Asn 100 105 110

Phe Ile Arg Phe Leu Gln Pro Tyr Asn Ala Ser His Leu Tyr Val Cys 115 120 125

Gly Thr Tyr Ala Phe Gln Pro Lys Cys Thr Tyr Val Asn Met Leu Thr 130 135 140

Phe Thr Leu Glu His Gly Glu Phe Glu Asp Gly Lys Gly Lys Cys Pro 145 150 155 160

Tyr Asp Pro Ala Lys Gly His Ala Gly Leu Leu Val Asp Gly Glu Leu 165 170 175

Tyr Ser Ala Thr Leu Asn Asn Phe Leu Gly Thr Glu Pro Ile Ile Leu 180 185 190

Arg Asn Met Gly Pro His His Ser Met Lys Thr Glu Tyr Leu Ala Phe 195 200 205

Trp Leu Asn Glu Pro His Phe Val Gly Ser Ala Tyr Val Pro Glu Ser 210 215 220

Val Gly Ser Phe Thr Gly Asp Asp Asp Lys Val Tyr Phe Phe Phe Arg 225 230 235 240

Glu Arg Ala Val Glu Ser Asp Cys Tyr Ala Glu Gln Val Val Ala Arg



245 250 255

Val Ala Arg Val Cys Lys Gly Asp Met Gly Gly Ala Arg Thr Leu Gln 260 265 270

Arg Lys Trp Thr Thr Phe Leu Lys Ala Arg Leu Ala Cys Ser Ala Pro 275 280 285

Asn Trp Gln Leu Tyr Phe Asn Gln Leu Gln Ala Met His Thr Leu Gln 290 295 300

Asp Thr Ser Trp His Asn Thr Thr Phe Phe Gly Val Phe Gln Ala Gln 305 310 315 320

Trp Gly Asp Met Tyr Leu Ser Ala Ile Cys Glu Tyr Gln Leu Glu Glu 325 330 335

Ile Gln Arg Val Phe Glu Gly Pro Tyr Lys Glu Tyr His Glu Glu Ala 340 345 350

Gln Lys Trp Asp Arg Tyr Thr Asp Pro Val Pro Ser Pro Arg Pro Gly
355 360 365

Ser Cys Ile Asn Asn Trp His Arg Arg His Gly Tyr Thr Ser Ser Leu 370 375 380

Glu Leu Pro Asp Asn Ile Leu Asn Phe Val Lys Lys His Pro Leu Met 385 390 395 400

Glu Glu Gln Val Gly Pro Arg Trp Ser Arg Pro Leu Leu Val Lys Lys
405 410 415

Gly Thr Asn Phe Thr His Leu Val Ala Asp Arg Val Thr Gly Leu Asp 420 425 430

Gly Ala Thr Tyr Thr Val Leu Phe Ile Gly Thr Gly Asp Gly Trp Leu 435 440 445

Leu Lys Ala Val Ser Leu Gly Pro Trp Val His Leu Ile Glu Glu Leu 450 455 460

Gln Leu Phe Asp Gln Glu Pro Met Arg Ser Leu Val Leu Ser Gln Ser 465 470 475 480

Lys Lys Leu Leu Phe Ala Gly Ser Arg Ser Gln Leu Val Gln Leu Pro 485 490 495

Val Ala Asp Cys Ile Lys Tyr Arg Ser Cys Ala Asp Cys Val Leu Ala 500 505 510

Arg Asp Pro Tyr Cys Ala Trp Ser Val Asn Thr Ser Arg Cys Val Ala
515 520 525

Val Gly Gly His Ser Gly Ser Leu Leu Ile Gln His Val Met Thr Ser 530 535 540

Asp Thr Ser Gly Ile Cys Asn Leu Arg Gly Ser Lys Lys Val Arg Pro



Cys Leu Leu Pro Val Gln Gly Trp Glu Arg Leu Cys Glu Gly Lys Lys 595 600 605

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cag ctg gag atg gcg gac acg aga tcc gtg cac gag act agg ttt gag 144 Gln Leu Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu 35 40 45

gcg gcc gtg aag gtg atc cag agt ttg ccg aag aat gat tca ttc cag 192 Ala Ala Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln 50 55 60

cca aca aat gaa atg atg ctt aaa ttt tat agc ttc tat aag cag gca 240 Pro Thr Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala 65 70 75

act gaa gga ccc tgt aaa ctt tca agg cct gga ttt tgg gat cct att 288 Thr Glu Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile 80 85 90

									gat Asp			336
 _	_	_			_	_	_	_	aag Lys		_	384
									cgt Arg			432
									agg Arg 155			480
									tta Leu			528
									gtt Val			576
									gaa Glu			624
									aag Lys			672
									gtc Val 235			720
Asp	Lys		Gly	Phe	Gln	Āsp		Gln	gac Asp			768
									aag Lys			816
									att Ile			864
									cag Gln			912
									gaa Glu 315			960

					•										1000
	_	_		gac Asp	_		_							_	1008
				cat His 340											1056
				gta Val											1104
				gaa Glu											1152
				agc Ser											1200
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				gga Gly 420											1296
_			_	 ggc											1344
				gtg Val											1392
				cag Gln											1440
				aca Thr	_	_		_		_				_	1488
				ccc Pro 500											1536
-				ttt Phe		_	-		-						1584
	_		_	aaa Lys			tgag	gaaa	at <u>c</u>	ıgtgt	tttc	c to	aaga	ıagac	1638

D'

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Glu Met Ala Asp Thr Arg Ser Val His Glu Thr Arg Phe Glu Ala Ala 35 40 45

Val Lys Val Ile Gln Ser Leu Pro Lys Asn Asp Ser Phe Gln Pro Thr
50 55 60

Asn Glu Met Met Leu Lys Phe Tyr Ser Phe Tyr Lys Gln Ala Thr Glu 65 70 75 80

Gly Pro Cys Lys Leu Ser Arg Pro Gly Phe Trp Asp Pro Ile Gly Arg 85 90 95

Tyr Lys Trp Asp Ala Trp Ser Ser Leu Gly Asp Met Thr Lys Glu Glu
100 105 110

Ala Met Ile Ala Tyr Val Glu Glu Met Lys Lys Ile Ile Glu Thr Met 115 120 125

Pro Met Thr Glu Lys Val Glu Glu Leu Leu Arg Val Ile Gly Pro Phe 130 135 140

Tyr Glu Ile Val Glu Asp Lys Lys Ser Gly Arg Ser Ser Asp Ile Thr 145 150 155 160

Ser Val Arg Leu Glu Lys Ile Ser Lys Cys Leu Glu Asp Leu Gly Asn



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Val Leu Thr	Ser Thr 180	Pro As	sn Ala	Lys 185	Thr	Val	Asn	Gly	Lys 190	Ala	Glu
Ser Ser Asp 195	Ser Gly	Ala G	lu Ser 200	Glu	Glu	Glu	Glu	Ala 205	Gln	Glu	Glu
Val Lys Gly 210	Ala Glu	Gln Se	_	Asn	Asp	Lys	Lys 220	Met	Met	Lys	Lys
Ser Ala Asp 225	His Lys	Asn Le	eu Glu	Val	Ile	Val 235	Thr	Asn	Gly	Tyr	Asp 240
Lys Asp Gly	Phe Val 245	Gln As	sp Ile	Gln	Asn 250	Asp	Ile	His	Ala	Ser 255	Ser
Ser Leu Asn	Gly Arg 260	Ser Th	ır Glu	Glu 265	Val	Lys	Pro	Ile	Asp 270	Glu	Asn
Leu Gly Gln 275	Thr Gly	Lys Se	er Ala 280	Val	Cys	Ile	His	Gln 285	Asp	Ile	Asn
Asp Asp His 290	Val Glu	Asp Va		Gly	Ile	Gln	His 300	Leu	Thr	Ser	Asp
Ser Asp Ser 305	Glu Val	Tyr Cy 310	/s Asp	Ser	Met	Glu 315	Gln	Phe	Gly	Gln	Glu 320
Glu Ser Leu	Asp Ser 325	Phe Th	ır Ser	Asn	Asn 330	Gly	Pro	Phe	Gln	Tyr 335	Tyr
Leu Gly Gly	His Ser 340	Ser G	ln Pro	Met 345	Glu	Asn	Ser	Gly	Phe 350	Arg	Glu
Asp Ile Gln 355	Val Pro	Pro G	y Asn 360	Gly	Asn	Ile	Gly	Asn 365	Met	Gln	Val
Val Ala Val 370	Glu Gly	Lys G		Val	Lys	His	Gly 380	Gly	Glu	Asp	Gly
Arg Asn Asn 385	Ser Gly	Ala Pi 390	o His	Arg	Glu	Lys 395	Arg	Gly	Gly	Glu	Thr 400
Asp Glu Phe	Ser Asn 405	Val Aı	g Arg	Gly	Arg 410	Gly	His	Arg	Met	Gln 415	His
Leu Ser Glu	Gly Thr 420	Lys Gl	y Arg	Gln 425	Val	Gly	Ser	Gly	Gly 430	Asp	Gly
Glu Arg Trp 435	Gly Ser	Asp Ar	g Gly 440	Ser	Arg	Gly	Ser	Leu 445	Asn	Glu	Gln
Ile Ala Leu 450	Val Leu	Met Ar	-	Gln	Glu	Asp	Met 460	Gln	Asn	Val	Leu
Gln Arg Leu	Gln Lys	Leu Gl	u Thr	Leu	Thr	Ala	Leu	Gln	Ala	Lys	Ser

465	470	475	480
Ser Thr Ser Thr Leu 485	Gln Thr Ala Pro	Gln Pro Thr Se	er Gln Arg Pro 495
Ser Trp Trp Pro Phe 500	Glu Met Ser Pro		nr Phe Ala Ile 510
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ctgttt	sacce eccaagagee ecgageeecg e	э т
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(213)	ATTITITIAL SEQUENCE	
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